1643

```
        RAW SEQUENCE LISTING                    DATE: 06/06/2000
        PATENT APPLICATION:   US/09/501,171A    TIME: 15:18:37
```

```
        Input Set  : A:\Seqlist.txt
        Output Set: N:\CRF3\06062000\I501171A.raw
```

```
        4 <110> APPLICANT: St. George-Hyslop, Peter H.
        5         Fraser, Paul E.
        7 <120> TITLE OF INVENTION: Proteins Related to Neuronal
        8         Regeneration and Uses Thereof
       10 <130> FILE REFERENCE: 1034/1F811
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/501,171A
C--> 12 <141> CURRENT FILING DATE: 2000-02-09
       12 <160> NUMBER OF SEQ ID NOS: 6
       14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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      233 <210> SEQ ID NO: 4
      234 <211> LENGTH: 1225
      235 <212> TYPE: PRT
      236 <213> ORGANISM: human
      238 <400> SEQUENCE: 4
      239   Met Phe Ala Arg Lys Pro Pro Gly Ala Ala Pro Leu Gly Ala Met Pro
      240   1               5                   10                  15
      241   Val Pro Asp Gln Pro Ser Ser Ala Ser Glu Lys Thr Ser Ser Leu Ser
      242               20                  25                  30
      243   Pro Gly Leu Asn Thr Ser Asn Gly Asp Gly Ser Glu Thr Glu Thr Thr
      244           35                  40                  45
      245   Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
      246       50                  55                  60
      247   Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
      248   65                  70                  75                  80
      249   Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Met Ser
      250                   85                  90                  95
      251   Ser Ala Glu Glu Gln Phe Gln Trp Gln Ser Gln Asp Gly Gln Lys Asp
      252               100                 105                 110
      253   Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
      254           115                 120                 125
      255   Arg Ser Leu Gln Glu Ser Gly Ile Leu Asp Pro Gln Asp Tyr Ser Thr
      256           130                 135                 140
      257   Gly Glu Arg Pro Ser Leu Leu Ser Gln Ser Ala Leu Gln Leu Asn Ser
      258   145                 150                 155                 160
      259   Lys Pro Glu Gly Ser Phe Gln Tyr Pro Ala Ser Tyr His Ser Asn Gln
      260                   165                 170                 175
      261   Thr Leu Ala Leu Gly Glu Thr Thr Pro Ser Gln Leu Pro Ala Arg Gly
      262               180                 185                 190
      263   Thr Gln Ala Arg Ala Thr Gly Gln Ser Phe Ser Gln Gly Thr Thr Ser
      264           195                 200                 205
      265   Arg Ala Gly His Leu Ala Gly Pro Glu Pro Ala Pro Pro Pro Pro Pro
      266           210                 215                 220
      267   Pro Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/501,171A

DATE: 06/06/2000
TIME: 15:18:37

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\06062000\I501171A.raw

```
268  225                   230                   235                   240
269  Pro Asp Ala Pro Pro Ala Ala Ala Ala Ala Leu Tyr Tyr Ser Ser
270              245               250               255
271  Ser Thr Leu Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Ala Ala Pro
272          260               265               270
273  Gln Gly Gly Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu
274          275               280               285
275  Gly Ala Thr Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro
276          290               295               300
277  Ser Arg Leu Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val
278  305               310               315               320
279  Val Ser Ser Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr
280              325               330               335
281  Val Gln Ser Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr
282          340               345               350
283  Ile Gly Thr Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala
284          355               360               365
285  Ser Glu Gln Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr
286          370               375               380
287  Leu Gln Arg Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser
288  385               390               395               400
289  Ser Gln His Gly His Leu Gly Pro Glu Leu Arg Ala Leu Gln Ser Pro
290              405               410               415
291  Glu His His Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro
292          420               425               430
293  Pro Met Arg Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala
294          435               440               445
295  His Thr Gly Thr Tyr Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val
296          450               455               460
297  Asp Ser Val Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn
298  465               470               475               480
299  Ala Ala Ala Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala
300              485               490               495
301  Ser Asn Tyr Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Pro Ser Val
302          500               505               510
303  Glu Ser Pro Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr
304          515               520               525
305  Leu Ala Arg Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu
306          530               535               540
307  Phe Gly Trp Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln
308  545               550               555               560
309  His Gln Phe Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His
310              565               570               575
311  Leu Cys Phe Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly
312          580               585               590
313  Gly Ile Gln Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val
314          595               600               605
315  His Arg Ser Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala
316          610               615               620
```

```
317  Asn Asp Asp Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala
318  625             630             635             640
319  Leu Val Arg Leu Leu Arg Lys Thr Thr Asp Leu Glu Ile Arg Glu Leu
320              645             650             655
321  Val Thr Gly Val Leu Trp Asn Leu Ser Ser Cys Asp Ala Leu Lys Met
322          660             665             670
323  Pro Ile Ile Gln Asp Ala Leu Ala Val Leu Thr Asn Ala Val Ile Ile
324      675             680             685
325  Pro His Ser Gly Trp Glu Asn Ser Pro Leu Gln Asp Arg Lys Ile
326      690             695             700
327  Gln Leu His Ser Ser Gln Val Leu Arg Asn Ala Thr Gly Cys Leu Arg
328  705             710             715             720
329  Asn Val Ser Ser Ala Gly Glu Glu Ala Arg Arg Arg Met Arg Glu Cys
330              725             730             735
331  Asp Gly Leu Thr Asp Ala Leu Leu Tyr Val Ile Gln Ser Ala Leu Gly
332          740             745             750
333  Ser Ser Glu Ile Asp Ser Lys Thr Val Glu Asn Cys Val Cys Ile Leu
334      755             760             765
335  Arg Asn Leu Ser Tyr Arg Leu Ala Ala Glu Thr Ser Gln Gly Gln His
336      770             775             780
337  Met Gly Thr Asp Glu Leu Asp Gly Leu Leu Cys Gly Glu Ala Asn Gly
338  785             790             795             800
339  Lys Asp Ala Glu Ser Ser Gly Cys Trp Gly Lys Lys Lys Lys Lys Lys
340              805             810             815
341  Lys Ser Gln Asp Gln Trp Asp Gly Val Gly Pro Leu Pro Asp Cys Ala
342          820             825             830
343  Glu Pro Pro Lys Gly Ile Gln Met Leu Trp His Pro Ser Ile Val Lys
344      835             840             845
345  Pro Tyr Leu Thr Leu Leu Ser Glu Cys Ser Asn Pro Asp Thr Leu Glu
346      850             855             860
347  Gly Ala Ala Gly Ala Leu Gln Asn Leu Ala Ala Gly Ser Trp Lys Trp
348  865             870             875             880
349  Ser Val Tyr Ile Arg Ala Ala Val Arg Lys Glu Lys Gly Leu Pro Ile
350              885             890             895
351  Leu Val Glu Leu Leu Arg Ile Asp Asn Asp Arg Val Val Cys Ala Val
352          900             905             910
353  Ala Thr Ala Leu Arg Asn Met Ala Leu Asp Val Arg Asn Lys Glu Leu
354      915             920             925
355  Ile Gly Lys Tyr Ala Met Arg Asp Leu Val His Arg Leu Pro Gly Gly
356      930             935             940
357  Asn Asn Ser Asn Asn Thr Ala Ser Lys Ala Met Ser Asp Asp Thr Val
358  945             950             955             960
359  Thr Ala Val Cys Cys Thr Leu His Glu Val Ile Thr Lys Asn Met Glu
360              965             970             975
361  Asn Ala Lys Ala Leu Arg Asp Ala Gly Gly Ile Glu Lys Leu Val Gly
362          980             985             990
363  Ile Ser Lys Ser Lys Gly Asp Lys His Ser Pro Lys Val Val Lys Ala
364      995             1000            1005
365  Ala Ser Gln Val Leu Asn Ser Met Trp Gln Tyr Arg Asp Leu Arg Ser
```

RAW SEQUENCE LISTING   DATE: 06/06/2000
PATENT APPLICATION: US/09/501,171A   TIME: 15:18:37

```
          Input Set : A:\Seqlist.txt
          Output Set: N:\CRF3\06062000\I501171A.raw

     366      1010                1015                1020
     367  Leu Tyr Lys Lys Asp Gly Trp Ser Gln Tyr His Phe Val Ala Ser Ser
E--> 368  1025                1030                1035            104
     369  Ser Thr Ile Glu Arg Asp Arg Gln Arg Pro Tyr Ser Ser Ser Arg Thr
     370              1045                1050                1055
     371  Pro Ser Ile Ser Pro Val Arg Val Ser Pro Asn Asn Arg Ser Ala Ser
     372              1060                1065                1070
     373  Ala Pro Ala Ser Pro Arg Glu Met Ile Ser Leu Lys Glu Arg Lys Thr
     374          1075                1080                1085
     375  Asp Tyr Glu Cys Thr Gly Ser Asn Ala Thr Tyr His Gly Ala Lys Gly
     376          1090                1095                1100
     377  Glu His Thr Ser Arg Lys Asp Ala Met Thr Ala Gln Asn Thr Gly Ile
E--> 378  1105                1110                1115            112
     379  Ser Thr Leu Tyr Arg Asn Ser Tyr Gly Ala Pro Ala Glu Asp Ile Lys
     380              1125                1130                1135
     381  His Asn Gln Val Ser Ala Gln Pro Val Pro Gln Glu Pro Ser Arg Lys
     382              1140                1145                1150
     383  Asp Tyr Glu Thr Tyr Gln Pro Phe Gln Asn Ser Thr Arg Asn Tyr Asp
     384          1155                1160                1165
     385  Glu Ser Phe Phe Glu Asp Gln Val His His Arg Pro Pro Ala Ser Glu
     386          1170                1175                1180
     387  Tyr Thr Met His Leu Gly Leu Lys Ser Thr Gly Asn Tyr Val Asp Phe
E--> 388  1185                1190        ·        1195            120
     389  Tyr Ser Ala Ala Arg Pro Tyr Ser Glu Leu Asn Tyr Glu Thr Ser His
     390              1205                1210                1215
     391  Tyr Pro Ala Ser Pro Asp Ser Trp Val
     392              1220                1225
     485  <210> SEQ ID NO: 6
     486  <211> LENGTH: 1247
     487  <212> TYPE: PRT
     488  <213> ORGANISM: mouse
     490  <400> SEQUENCE: 6
     491  Met Phe Ala Arg Lys Gln Ser Gly Ala Ala Pro Phe Gly Ala Met Pro
     492  1               5                   10                  15
     493  Val Pro Asp Gln Pro Pro Ser Ala Ser Glu Lys Asn Ser Ser Leu Ser
     494              20                  25                  30
     495  Pro Gly Leu Asn Thr Ser Asn Gly Asp Gly Ser Glu Thr Glu Thr Thr
     496          35                  40                  45
     497  Ser Ala Ile Leu Ala Ser Val Lys Glu Gln Glu Leu Gln Phe Glu Arg
     498          50                  55                  60
     499  Leu Thr Arg Glu Leu Glu Ala Glu Arg Gln Ile Val Ala Ser Gln Leu
     500  65                  70                  75                  80
     501  Glu Arg Cys Lys Leu Gly Ser Glu Thr Gly Ser Met Ser Ser Ile Ser
     502                  85                  90                  95
     503  Ser Ala Gly Glu Gln Phe His Trp Gln Thr Gln Asp Gly Gln Lys Asp
     504              100                 105                 110
     505  Ile Glu Asp Glu Leu Thr Thr Gly Leu Glu Leu Val Asp Ser Cys Ile
     506          115                 120                 125
     507  Arg Ser Leu Gln Glu Ser Gly Ile Leu Asp Pro Gln Asp Tyr Ser Thr
```

RAW SEQUENCE LISTING   DATE: 06/06/2000
PATENT APPLICATION: US/09/501,171A   TIME: 15:18:37

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\06062000\I501171A.raw

```
508        130                    135                    140
509   Ser Glu Arg Pro Ser Leu Leu Ser Gln Ser Ala Leu Gln Leu Asn Ser
510   145                    150                    155                    160
511   Lys Pro Glu Gly Ser Phe Gln Tyr Pro Ala Ser Tyr His Ser Asn Gln
512                    165                    170                    175
513   Thr Leu Ala Leu Gly Asp Thr Ala Pro Ser Gln Leu Pro Ala Arg Ser
514                    180                    185                    190
515   Thr Gln Ala Arg Ala Ala Gly Gln Ser Phe Ser Gln Gly Thr Thr Gly
516             195                    200                    205
517   Arg Ala Gly His Leu Ala Gly Ser Glu Pro Ala Pro Pro Pro Pro Pro
518             210                    215                    220
519   Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu Pro
520   225                    230                    235                    240
521   Asp Ala Pro Pro Ala Ala Ala Ala Leu Tyr Tyr Ser Ser Ser Thr Leu
522                    245                    250                    255
523   Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Thr Thr Thr Gln Gly Gly
524                    260                    265                    270
525   Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu Gly Ala Ala
526             275                    280                    285
527   Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro Ser Arg Leu
528             290                    295                    300
529   Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val Val Ser Ser
530   305                    310                    315                    320
531   Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr Val Gln Ser
532                    325                    330                    335
533   Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr Ile Gly Thr
534                    340                    345                    350
535   Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala Ser Glu Gln
536             355                    360                    365
537   Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr Leu Gln Arg
538             370                    375                    380
539   Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser Ser Gln His
540   385                    390                    395                    400
541   Gly His Leu Ala Pro Glu Leu Arg Ala Leu Gln Ser Pro Glu His His
542                    405                    410                    415
543   Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro Pro Met Arg
544                    420                    425                    430
545   Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala His Thr Gly
546             435                    440                    445
547   Thr Phe Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val Asp Ser Val
548             450                    455                    460
549   Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn Ala Ala Ala
550   465                    470                    475                    480
551   Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala Ser Asn Tyr
552             485                    490                    495
553   Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Ala Ser Val Asp Ser Pro
554             500                    505                    510
555   Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr Leu Ala Arg
556             515                    520                    525
```

```
557   Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu Phe Gly Trp
558       530                 535                 540
559   Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln His Gln Phe
560   545                 550                 555                 560
561   Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His Leu Cys Phe
562                   565                 570                 575
563   Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly Gly Ile Gln
564               580                 585                 590
565   Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val His Arg Ser
566               595                 600                 605
567   Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala Asn Asp Asp
568       610                 615                 620
569   Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala Leu Val Arg
570   625                 630                 635                 640
571   Leu Leu Arg Lys Thr Thr Asp Leu Glu Ile Arg Glu Leu Val Thr Gly
572               645                 650                 655
573   Val Leu Trp Asn Leu Ser Ser Cys Asp Ala Leu Lys Met Pro Ile Ile
574               660                 665                 670
575   Gln Asp Ala Leu Ala Val Leu Thr Asn Ala Val Ile Ile Pro His Ser
576       675                 680                 685
577   Gly Trp Glu Asn Ser Pro Leu Gln Asp Asp Arg Lys Ile Gln Leu His
578       690                 695                 700
579   Ser Ser Gln Val Leu Arg Asn Ala Thr Gly Cys Leu Arg Asn Val Ser
580   705                 710                 715                 720
581   Ser Ala Gly Glu Glu Ala Arg Arg Arg Met Arg Glu Cys Asp Gly Leu
582               725                 730                 735
583   Thr Asp Ala Leu Leu Tyr Val Ile Gln Ser Ala Leu Gly Ser Ser Glu
584               740                 745                 750
585   Ile Asp Ser Lys Thr Val Glu Asn Cys Val Cys Ile Leu Arg Asn Leu
586               755                 760                 765
587   Ser Tyr Arg Leu Ala Ala Glu Thr Ser Gln Gly Gln His Met Gly Thr
588       770                 775                 780
589   Asp Glu Leu Asp Gly Leu Leu Cys Gly Glu Thr Asn Gly Lys Asp Thr
590   785                 790                 795                 800
591   Glu Ser Ser Gly Cys Trp Gly Lys Lys Lys Lys Lys Lys Ser Gln
592               805                 810                 815
593   Asp Gln Trp Asp Gly Val Gly Pro Leu Pro Asp Cys Ala Glu Pro Pro
594               820                 825                 830
595   Lys Gly Ile Gln Met Leu Trp His Pro Ser Ile Val Lys Pro Tyr Leu
596               835                 840                 845
597   Thr Leu Leu Ser Glu Cys Ser Asn Pro Asp Thr Leu Glu Gly Ala Ala
598       850                 855                 860
599   Gly Ala Leu Gln Asn Leu Ala Ala Gly Ser Trp Lys Gly Trp Ala Glu
600   865                 870                 875                 880
601   Asp Val Ala Gly Met Ala Tyr Ala Leu Arg Ser Leu Pro Glu Gly Ala
602               885                 890                 895
603   Pro Cys Leu Pro Gln Trp Ser Val Tyr Ile Arg Ala Ala Val Arg Lys
604               900                 905                 910
605   Glu Lys Gly Leu Pro Ile Leu Val Glu Leu Leu Arg Ile Asp Asn Asp
```

RAW SEQUENCE LISTING   DATE: 06/06/2000
PATENT APPLICATION: US/09/501,171A   TIME: 15:18:37

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\06062000\I501171A.raw

```
         606        915                920                925
         607    Arg Val Val Cys Ala Val Ala Thr Ala Leu Arg Asn Met Ala Leu Asp
         608        930                935                940
         609    Val Arg Asn Lys Glu Leu Ile Gly Lys Tyr Ala Met Arg Asp Leu Val
         610    945                950                955                960
         611    His Arg Leu Pro Gly Gly Asn Asn Ser Asn Asn Ser Gly Ser Lys Ala
         612                965                970                975
         613    Met Ser Asp Asp Thr Val Thr Ala Val Cys Cys Thr Leu His Glu Val
         614            980                985                990
         615    Ile Thr Lys Asn Met Glu Asn Ala Lys Ala Leu Arg Asp Ala Gly Gly
         616        995                1000               1005
         617    Ile Glu Lys Leu Val Gly Ile Ser Lys Ser Lys Gly Asp Lys His Ser
         618    1010               1015               1020
         619    Pro Lys Val Val Lys Ala Ala Ser Gln Val Leu Asn Ser Met Trp Gln
E--> 620    1025               1030               1035               104
         621    Tyr Arg Asp Leu Arg Ser Leu Tyr Lys Lys Asp Gly Trp Ser Gln Tyr
         622                1045               1050               1055
         623    His Phe Val Ala Ser Ser Ser Thr Ile Glu Arg Asp Arg Gln Arg Pro
         624            1060               1065               1070
         625    Tyr Ser Ser Ser Arg Thr Pro Ser Ile Ser Pro Val Arg Val Ser Pro
         626        1075               1080               1085
         627    Asn Asn Arg Ser Ala Ser Ala Pro Ala Ser Pro Arg Glu Met Ile Ser
         628        1090               1095               1100
         629    Leu Lys Glu Arg Lys Thr Asp Tyr Glu Ser Ala Gly Asn Asn Ala Thr
E--> 630    1105               1110               1115               112
         631    Tyr His Gly Thr Lys Gly Glu His Thr Ser Arg Lys Asp Thr Met Thr
         632                1125               1130               1135
         633    Ala Gln Asn Thr Gly Val Ser Thr Leu Tyr Arg Asn Ser Tyr Gly Ala
         634            1140               1145               1150
         635    Pro Ala Glu Asp Ile Lys Gln Asn Gln Val Ser Thr Gln Pro Val Pro
         636        1155               1160               1165
         637    Gln Glu Pro Ser Arg Lys Asp Tyr Glu Thr Tyr Gln Pro Phe Pro Asn
         638        1170               1175               1180
         639    Ser Thr Arg Asn Tyr Asp Glu Ser Phe Phe Glu Asp Gln Val His His
E--> 640    1185               1190               1195               120
         641    Arg Pro Pro Ala Ser Glu Tyr Thr Met His Leu Gly Leu Lys Ser Thr
         642                1205               1210               1215
         643    Gly Asn Tyr Val Asp Phe Tyr Ser Ala Ala Arg Pro Tyr Ser Glu Leu
         644            1220               1225               1230
         645    Asn Tyr Glu Thr Ser His Tyr Pro Ala Ser Pro Asp Ser Trp Val
         646        1235               1240               1245
```

VERIFICATION SUMMARY   DATE: 06/06/2000
PATENT APPLICATION: US/09/501,171A   TIME: 15:18:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\06062000\I501171A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:368 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:620 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6